

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 17:46:47 ; Search time 4900.12 Seconds
(without alignments)
16080.756 Million cell updates/sec

Title: US-10-018-786-6
Perfect score: 1818
Sequence: 1 atgcacacgcgtctctcc.....cgcatactctcgcctga 1818

Scoring table: IDENTITY NJC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_nm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_cm.*
21: em_cr.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
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26: em_ro.*
27: em_sts.*

- 28: em_un.*
29: em_vt.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pin.*
35: em_htg_rnd.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1818	100.0	1818	6 AX061805	AX061805 Sequence
2	1818	100.0	11629	1 AE012222	AE012222 Xanthomon
3	1203.4	66.2	11789	1 AE011667	AE011667 Xanthomon
c 4	1200.2	66.0	29208	1 AF499777	AF499777 Xanthomon
5	1196.6	65.8	1824	1 XANHRPALA	M99173 Xanthomonas
6	1196.6	65.8	1824	1 XCI33548	U33548 Xanthomonas
c 7	1180.6	64.9	8230	1 AY139029S1	AY139029 Xanthomon
c 8	1180.6	64.9	19304	1 AB045311	AB045311 Xanthomon
c 9	1180.6	64.9	23514	1 AY205561	AY205561 Xanthomon
c 10	1180.6	64.9	100258	1 AY055110	AY055110 Xanthomon
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c 15	467.2	25.7	197050	1 AL646081	AL646081 Ralstonia
16	358	19.7	23814	1 AF074878	AF074878 Burkholde
17	152.2	8.4	15231	1 AY166598	AY166598 Burkholde
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19	115.6	6.4	11557	1 AE004598	AE004598 Pseudomon
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21	100.6	5.3	34321	1 BX640429	BX640429 Bordetell
22	99	5.4	348624	1 BX640441	BX640441 Bordetell
23	97.6	5.4	1803	6 BD269173	BD269173 Vaccine.
24	97.6	5.4	1803	6 AX028410	AX028410 Sequence
25	97.6	5.4	35026	1 BPHYPLCRD	Y13383 Bordetella
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28	82.2	4.5	6176	1 EAU56662	U56662 Erwinia amy
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34 72.6 4.0 349980 6 AX770910 Sequence
35 72.2 4.0 20000 1 AF282857
c 36 71.8 3.9 125020 9 AF429315 Homo sapi
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c 38 68.6 3.8 28666 1 AY293288 Pectobact
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42 64.6 3.6 11120 1 AE004734 Pseudomon
c 43 63.8 3.5 16371 1 AF292566 Pseudomon
44 63.6 3.5 13197 1 AE004503 Pseudomon
45 63.4 3.5 11301 1 AE011699 Xanthomon

ALIGNMENTS

RESULT 1
LOCUS AX061805 1818 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 6 from Patent WO0078967.
ACCESSION AX061805
VERSION AX061805.1 GI:12539885

KEYWORDS Xanthomonas campestris
SOURCE Xanthomonas campestris
ORGANISM Xanthomonas campestris
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.

REFERENCE 1
AUTHORS Pierrard,J., Simon,J.L. and Chevallereau,P.
TITLE Avirulent xanthomonas-campestris strains producing xanthan
JOURNAL Patent: WO 0078967-A 6 28-DEC-2000;
RHODIA CHIMIE (FR)

FEATURES
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ORIGIN

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Matches 1818; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1801 CATATGCTCGGCGCTGA 1818

Db 1801 CATATGCTCGGCGCTGA 1818

RESULT 2
AE012222

LOCUS
DEFINITION
Xanthomonas campestris pv. campestris str. ATCC 33913, section 130 of 460 of the complete genome.
ACCESSION
AE012222 AE008922
VERSION
AE012222.1 GI:21112273
KEYWORDS
Xanthomonas campestris pv. campestris str. ATCC 33913
SOURCE
Xanthomonas campestris pv. campestris str. ATCC 33913
ORGANISM
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.
REFERENCE
1 (bases 1 to 11629)
da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R., Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C., Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardoso,J., Chamargo,F., Chapina,L.P., Cicarelli,R.M.B., Coutinho,L.L., Cursino-Santos,J.R., El-Dorry,H., Faris,J.B., Ferreira,A.J.S., Ferreira,R.C.C., Ferro,M.I.T., Formighieri,E.F., Franco,M.C., Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locali,E.C., Machado,M.A., Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meidanis,J., Menck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M., Okura,V.K., Oliveira,M.C., Oliveira,V.R., Pereira,Jr.,H.A., Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spindola,L.A.F., Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezra,R.I.D., Trindade dos Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and Kitajima,J.P.
TITLE
Comparison of the genomes of two Xanthomonas pathogens with differing host specificities
NATURE 417 (6887), 459-463 (2002)
JOURNAL
MEDLINE
PUBMED
12022145
12024217
REFERENCE
2 (bases 1 to 11629)
da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R., Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C., Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardoso,J., Cursino-Santos,J.R., El-Dorry,H., Faris,J.B., Ferreira,A.J.S., Ferreira,R.C.C., Ferro,M.I.T., Formighieri,E.F., Franco,M.C., Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locali,E.C., Machado,M.A., Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Meidanis,J., Menck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M., Okura,V.K., Oliveira,M.C., Oliveira,V.R., Pereira,Jr.,H.A., Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spindola,L.A.F., Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezra,R.I.D., Trindade dos Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and Kitajima,J.P.
TITLE
Direct Submission
JOURNAL
Submitted (28-NOV-2001) Departamento de Bioquímica, Universidade de Sao Paulo, Av. Prof. Lineu Prestes 746, Sao Paulo, SP 05508-900, Brazil
FEATURES
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Db 10703 AGCGGCGGTGAGCTGGCATCCGAGCGCGCGGTGATCGAAGCGGACCGCGGCAACCGG 10762
QY 1021 ATTCTCATTTCGCGACCGCGCGCGCGCGCTATGGCAGCTTATGCCAGAGTTCATCCAGAGT 1080
Db 10763 ATTCTCATTTCGCGACCGCGCGCGCGCGCTATGGCAGCTTATGCCAGAGTTCATCCAGAGT 10822
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Db QY 100.0%; Score 1818; DB 1; Length 11629;
Best Local Similarity 100.0%; Pred. No. 2.3e-247;
Matches 1818; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 301 TGGTATACGATGGCTCGGTGCTCAGATCTGGGGCGCGACGACCAAGATCGGACC 360

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Title: US-10-018-786-6
Perfect score: 1818
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1818	100.0	1818	5	ABL57894
2	97.6	5.4	1803	3	AAA64851
3	97.6	5.4	35026	3	AAA64890
4	72.6	4.0	1869	7	ACF71562
5	72.6	4.0	110000	7	ACF67367_47
6	72.6	4.0	110000	7	ACF65388_00
7	68	3.7	114955	2	AA53491

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Qy	1561	GACGGCGTGTGGCGGCAATACCGTCSATGGCATCCCGTCACTCCAGGAGATC	1620
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Qy	1681	ACCGATCAGACAGATCTGAACAGTCCCGGGGCTGTCCAGGATTCATGTGCGCAAC	1740
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Qy	1741	CTGTTCAGGATCCGACGAGCGGGTCCGGTTGCAGCGGTTGTTCTGTGACCCCG	1800
Db	11483	CTGTTCAGGATCCGACGAGCGGGTCCGGTTGCAGCGGTTGTTCTGTGACCCCG	11542
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Db	11543	CATATGCTCGCCCTGA	11560

Search completed: July 7, 2004, 23:54:54
Job time : 4910.12 secs

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9 62.2 3.4 2145 7 ABX94902
10 61.4 3.4 1752 7 ACA44288
11 61 3.4 2751 7 ACA38169
12 59 3.2 114955 2 AAX53491
13 56.8 3.1 2000 7 ADA71938
14 56.8 3.1 2481 2 AAT13557
15 56.8 3.1 2481 2 AAT73952
16 56.8 3.1 2481 2 AAT73952
17 56.8 3.1 2481 2 AAT73952
18 56.8 3.1 2571 3 AAX93974
19 56.8 3.1 2571 4 AAC86878
20 56.8 3.1 2571 5 AAH43701
21 56.6 3.1 1200 7 ACA26511
22 55.4 3.0 65140 4 RAD17184
23 55.4 3.0 125401 4 AAD17186
24 55.2 3.0 12588 2 AAQ63293
25 54.8 3.0 103599 4 ABX04971
26 54.4 3.0 30365 4 AAD20405
27 54.2 3.0 1746 7 ACA37403
28 54 3.0 1162 3 AAX9451
29 53.8 3.0 88421 6 AAL40781
30 53.6 2.9 1227 7 ADA70473
31 53 2.9 2000 7 ADA71938
32 52.8 2.9 113193 7 AAD54645
33 52.8 2.9 349980 6 ABQ81849
34 52.4 2.9 536 9 ADB68842
35 52.4 2.9 110000 4 AAI99683_08
36 52 2.9 16020 3 AAX39283
37 51.6 2.8 2331 4 AAS51455
38 51.6 2.8 2331 7 ACA19557
39 51.6 2.8 2772 7 ACA40420
40 51.6 2.8 15672 2 AAQ10613
41 51.6 2.8 110000 4 AAI99682_10
42 51.6 2.8 110000 4 AAI99683_10
43 51.2 2.8 34720 2 AAV30458_5
44 51.2 2.8 36165 2 AAV30459_5
45 51.2 2.8 110000 2 AAV30458_4

ALIGNMENTS

RESULT 1
ABL57894
ID ABL57894 standard; DNA; 1818 BP. 1
XX ABL57894;
AC ABL57894;
XX 11-SEP-2003 (revised)
DT 04-JUL-2002 (first entry)
XX
DE Partial hypersensitive reaction and pathogenicity, hrpA gene.
XX
KW Hypersensitive reaction and pathogenicity; hrpA; exo-polysaccharide;
XX xanthan gum; gene; ds.
XX

OS Xanthomonas campestris; pv vesicatoria.
XX WO200078967-A1.
XX 28-DEC-2000.
PD
PF 21-JUN-2000; 2000WO-FR001725.
XX
PR 22-JUN-1999; 99FR-0007963.
XX
XX (RHOD) RHODIA CHIM.
XX
XX Pierrard J, Simon J, Chevallereau P;
XX WPI; 2001-102725/11.
XX
PT New Xanthomonas campestris bacteria strains for use in production of exo-
PT polysaccharides are made non-virulent by inactivation of at least one
PT virulence gene.
XX
PS Claim 18; Page 26-27; 33pp; French.
XX
XX The present invention relates to new Xanthomonas campestris bacteria
CC strains made non-virulent by inactivation of at least one virulence gene
CC but which have retained the capacity to produce exo-polysaccharides
CC (preferably xanthan gum). One such virulence gene deleted to produce the
CC bacterial strains was the hrpA gene (Hypersensitive Reaction and
CC Pathogenicity). The hrp genes are essential for pathogenicity in plants.
CC The present sequence is a partial sequence of the hrpA, used in an
CC example from the invention. (Updated on 11-SEP-2003 to standardise OS
CC field)
XX
SQ Sequence 1818 BP; 306 A; 582 C; 602 G; 328 T; 0 U; 0 Other;
Query Match 100.0%; Score 1818; DB 5; Length 1818;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1818; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGGCATACGCTGTCTCCAGTTACCGCCCATCGACGCGCGCTTGGCGGCTGCTTG 60
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QY	1621	ACCAACGACGGCTCTCGTCAACGAGGGCGCACAGAGCTGTGATTCGCGGGTTATGCTCCGAC	1680			
Db	1621	ACCAACGACGGCTCTCGTCAACGAGGGCGCACAGAGCTGTGATTCGCGGGTTATGCTCCGAC	1680			
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Job time : 937.332 secs						

Search completed: July 7, 2004, 21:07:49
Job time : 537.332 secs

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 20:18:17 ; Search time 3500.23 Seconds
(without alignments)
15510.269 Million cell updates/sec

Title: US-10-018-786-6
Perfect score: 1815
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rpd:*
26: em_gss_png:*
27: em_gss_vrl:**

28: gb_gss1:*
29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	70	3.9	932	29	NS0072Q
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C 4	66.6	3.7	2481	28	BH614291 1C22/2B8
C 5	65.4	3.6	925	29	NS0091P
C 6	63	3.5	1101	29	NS0175Y
C 7	62.2	3.4	889	28	BZ571081
C 8	62.2	3.4	935	29	NS006XK
C 9	61.6	3.4	925	29	NS0091P
C 10	61	3.4	589	14	CB852504
C 11	61	3.4	1004	14	CD051228
C 12	61	3.4	1288	13	BQ678719
C 13	60.4	3.3	1151	14	CK210749
C 14	60	3.3	982	13	BX415111
C 15	59.6	3.3	723	14	CB854525
C 16	59.6	3.3	781	14	CB851140
C 17	59.6	3.3	982	13	BX415111
C 18	59.6	3.3	1085	28	BZ532651
C 19	59.4	3.3	935	29	NS006XK
C 20	59.2	3.3	1201	13	BX381961
C 21	59.2	3.3	1625	29	AG043477
C 22	58.4	3.2	1421	28	BZ569488
C 23	58.2	3.2	740	29	NS010QO
C 24	58.2	3.2	1250	29	AG043469
C 25	58	3.2	888	29	AG030591
C 26	57.8	3.2	928	29	AG054567
C 27	57.8	3.2	1452	29	AG032979
C 28	57.2	3.1	1311	12	BMS44820
C 29	56.6	3.1	921	28	AZ528613
C 30	56.6	3.1	932	29	NS0072Q
C 31	56.2	3.1	1150	13	BQ892481
C 32	56.2	3.1	1278	29	AG060116
C 33	56.2	3.1	1281	12	BQ852363
C 34	56.2	3.1	1342	29	BQ852343
C 35	56	3.1	1516	12	BQ809984
C 36	56	3.1	1610	28	BZ569386
C 37	55.8	3.1	1057	13	BX349688
C 38	55.8	3.1	1339	12	EM458211
C 39	55.8	3.1	1598	29	AG030579
C 40	55.4	3.0	927	13	BQ680645
C 41	55.4	3.0	1201	13	BX356664
C 42	55.4	3.0	1798	29	AGI71124
C 43	55.2	3.0	848	29	AG036341
C 44	55.2	3.0	895	29	AG064040
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Search completed: July 8, 2004, 01:54:08
Job time : 3505.23 secs